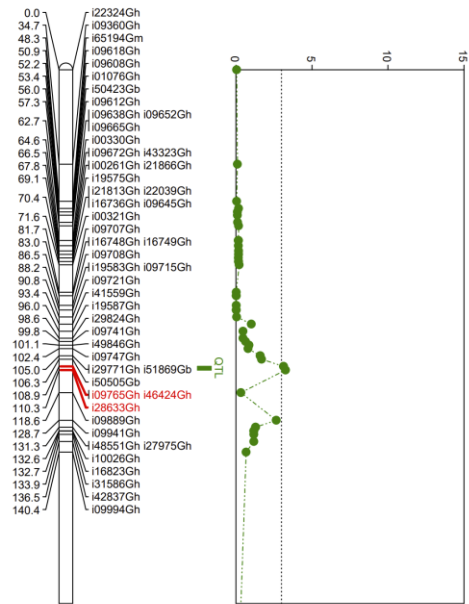
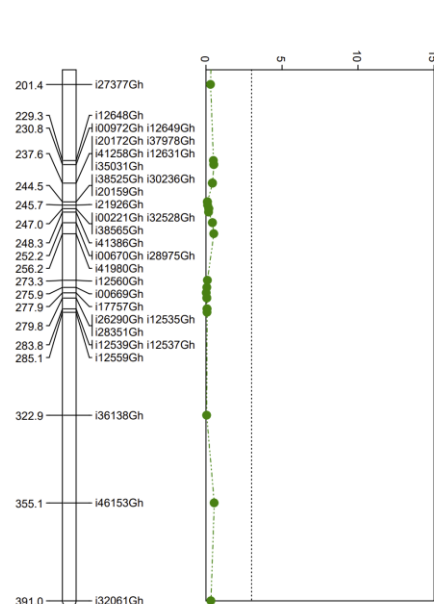


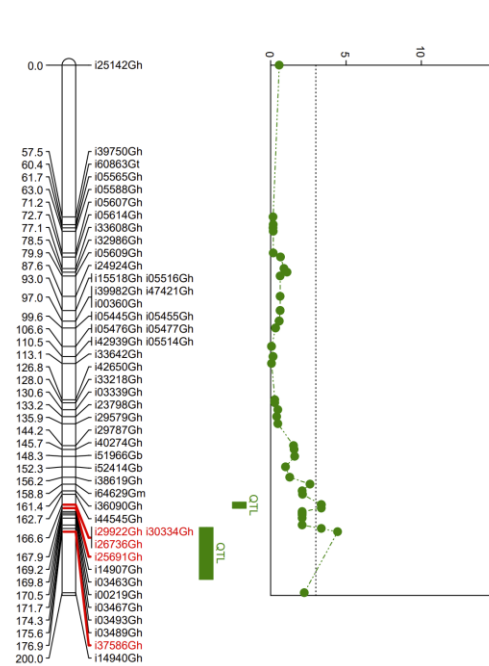
LG7 [1]



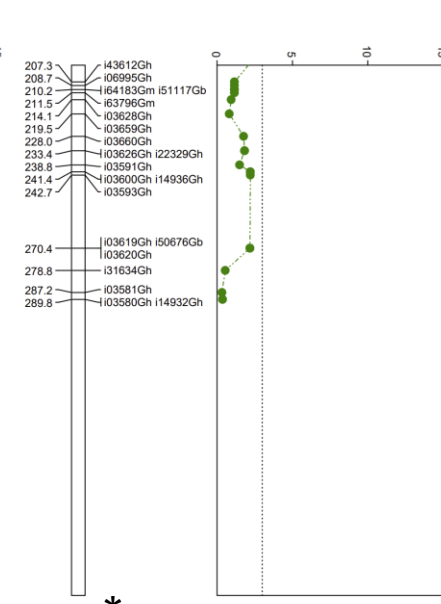
LG7 [2]



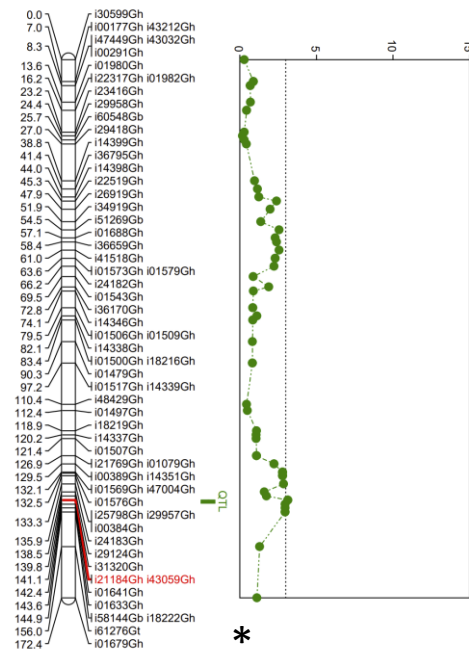
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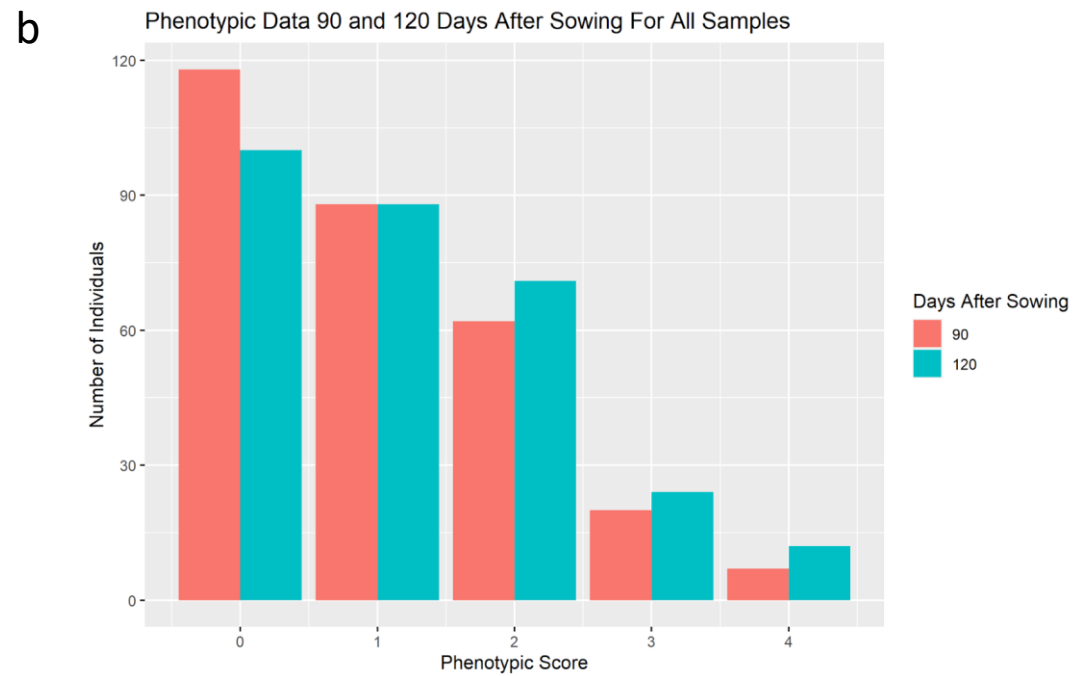
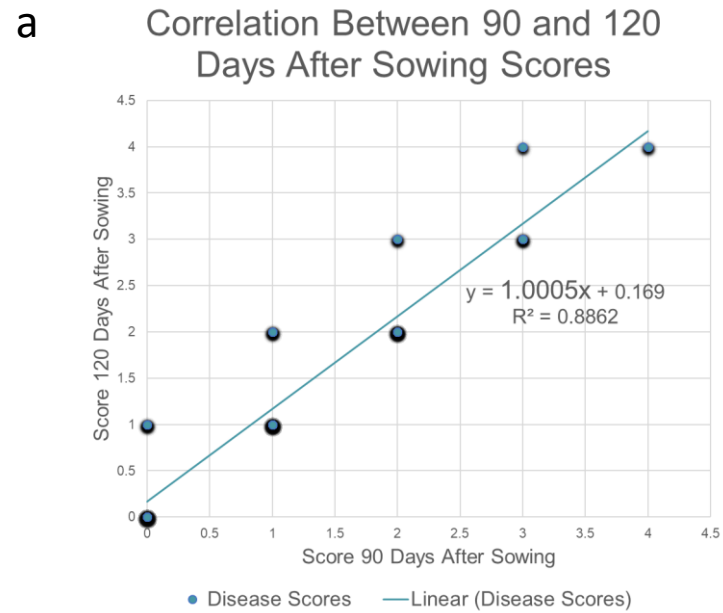


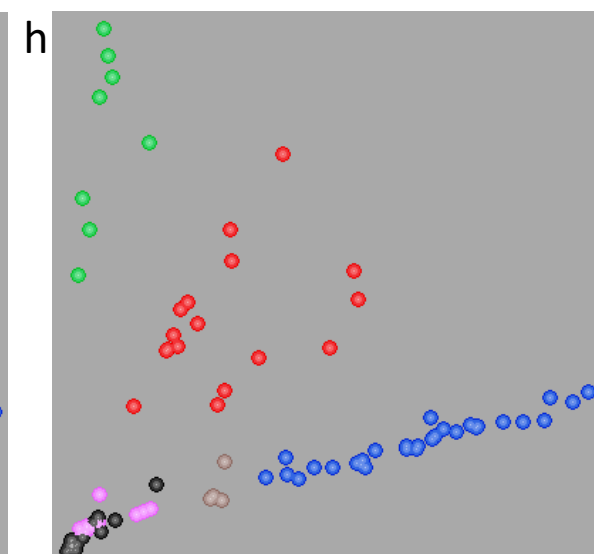
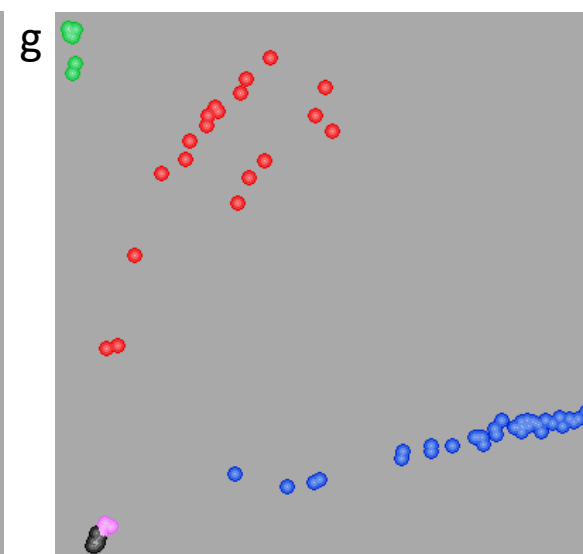
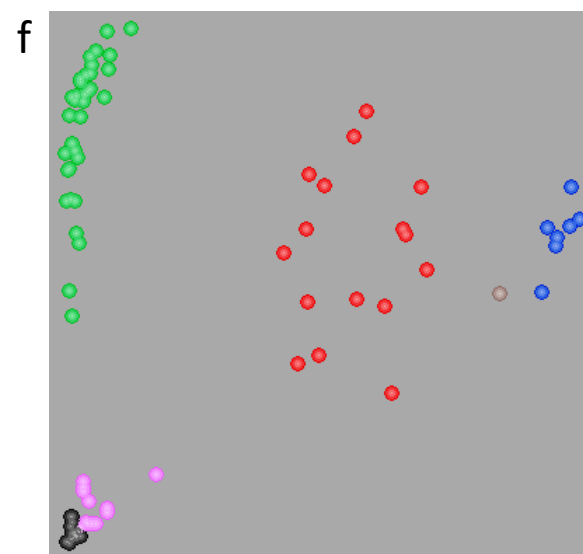
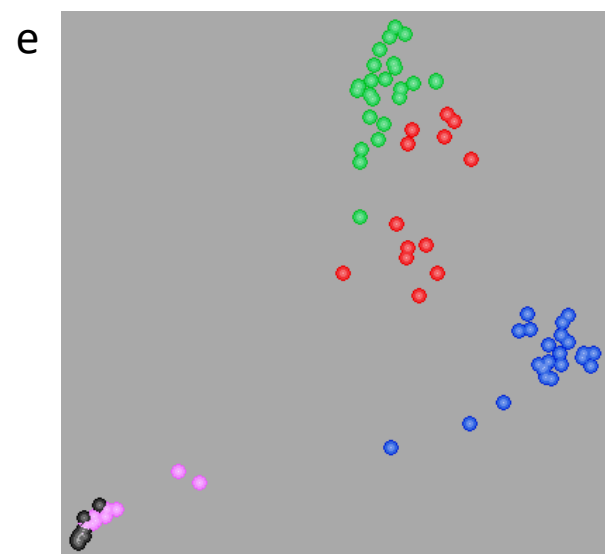
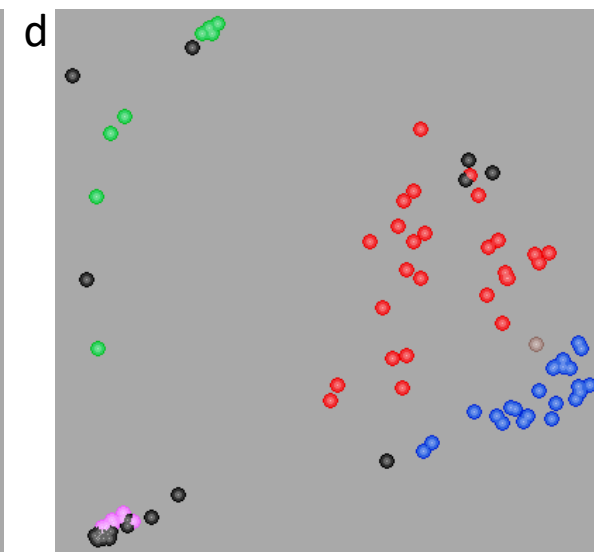
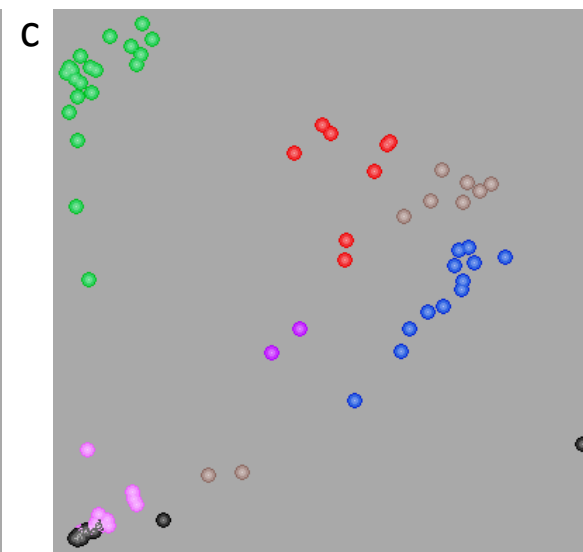
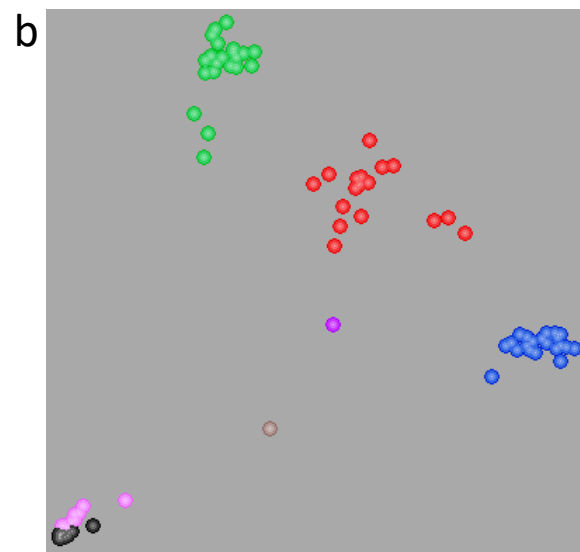
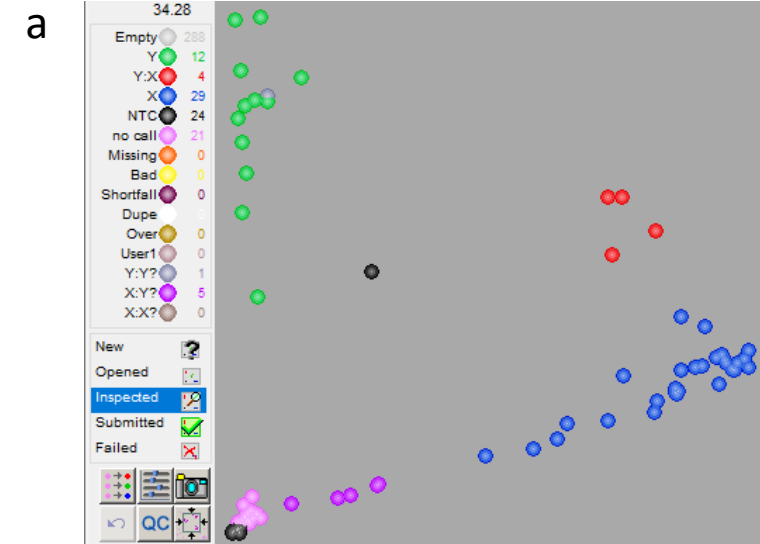
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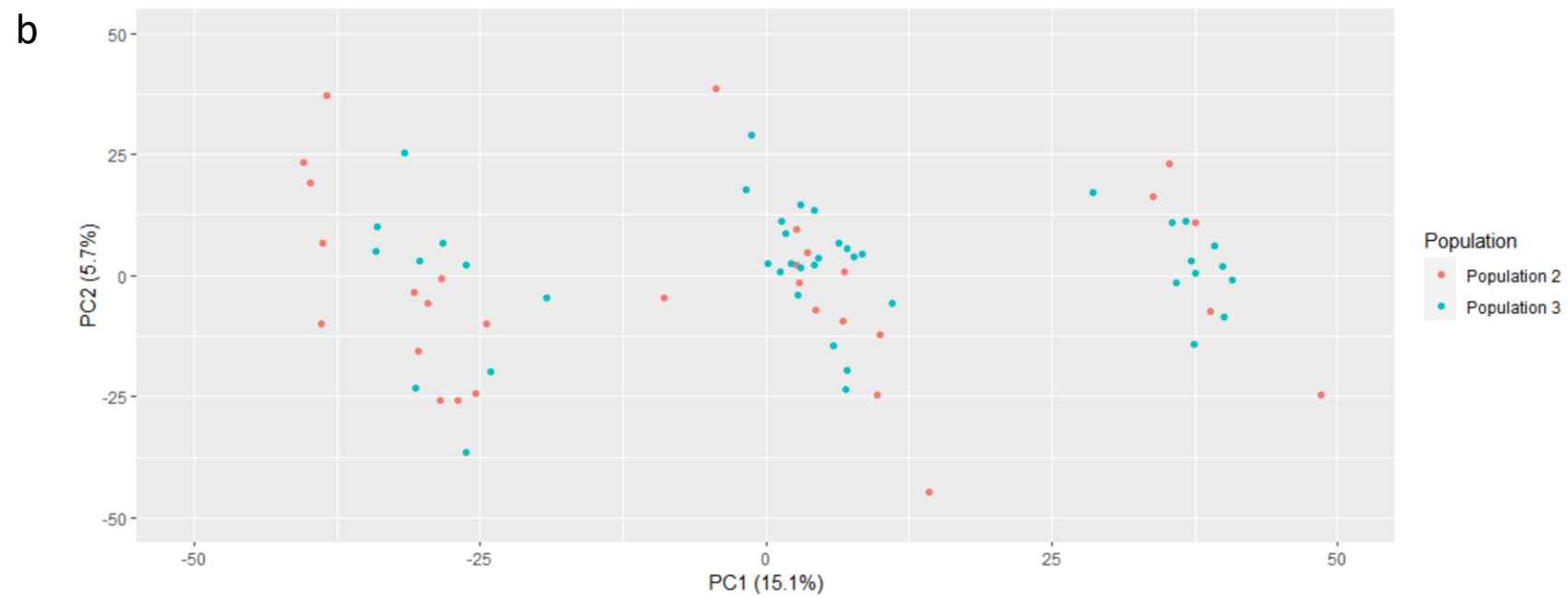
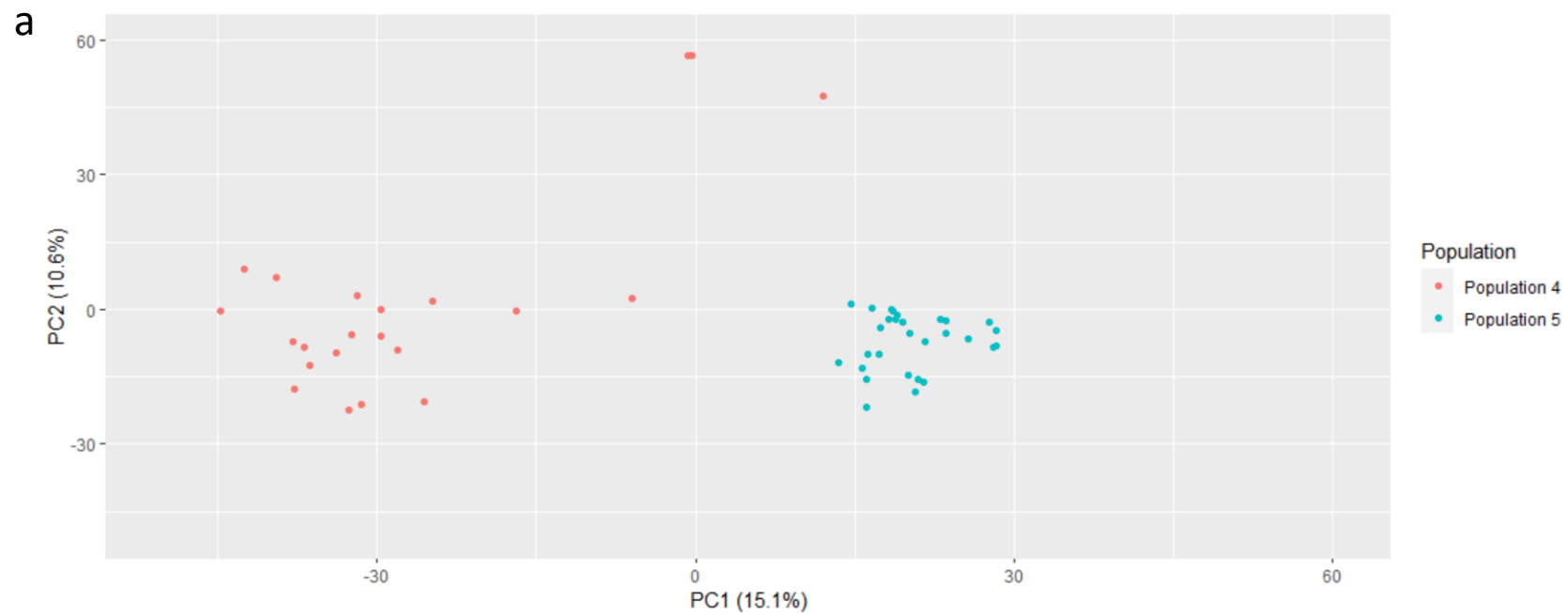


LG24

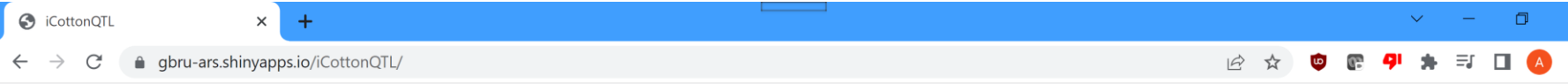








a



## iCottonQTL

Please cite: Schoonmaker, A. N., Hulse-Kemp, A. M., Youngblood, R. C., Rahmat, M. Z., Iqbal, M. A., Mehboob-ur-Rahman, Kochan, K. J., Scheffler, B. E., & Scheffler, J. A. Detecting Cotton Leaf Curl Virus Resistance Quantitative Trait Loci in Gossypium hirsutum and iCottonQTL a New R/Shiny App to Streamline Genetic Mapping in Cotton. Plants. 2023

This application is designed to streamline the downstream pre-processing of cotton genotyping data derived from the Illumina Array technology (CottonSNP63K). For additional details/tutorial on utilizing the application please see the github link

[Simple Steps Github Link](#)

[Extended Steps Github Link](#)

Generate Input File for JoinMap

CottonGen Upload Format

Example Final Report and example Sample List download available here:

[Example Files](#)

Choose TXT/CSV Final Report File(s)

Browse...

testShinyNoHeader.csv

Upload complete

Optional: Choose TXT File Containing List of Sample Names

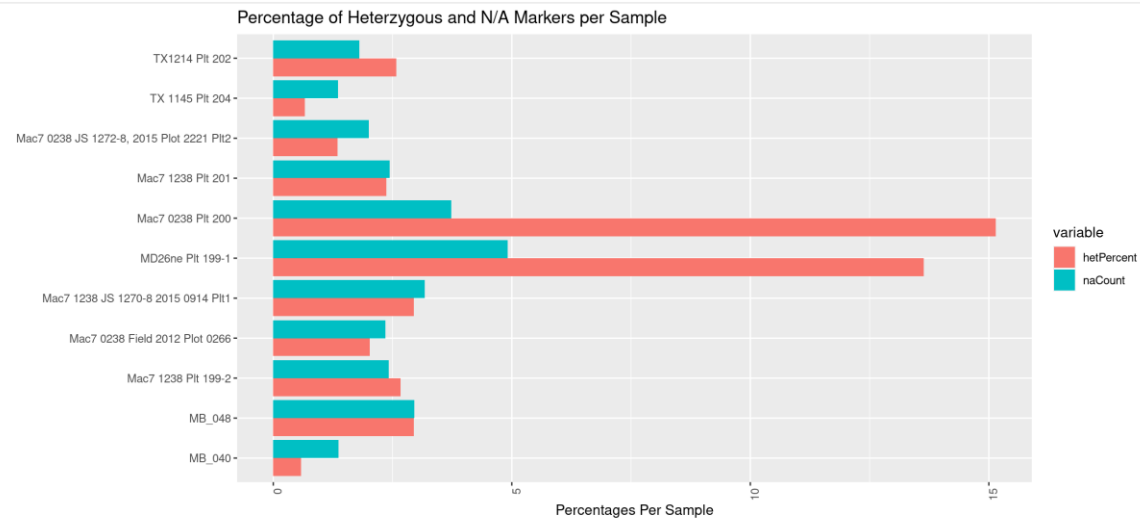
Browse...

No file selected

Select the Population Type:

F2

Please give the Maximum Missing Data Level per Sample



b

Please give the Maximum Missing Data Level per Sample (see graph) in decimal (ex: 100% is 1) \*This default will output all samples, user may change this, but in doing so may reduce the number of samples exported to the .loc file\*

1

Please give the Minimum Heterozygosity Level allowed per marker (calculated at the Overall Population Level) in decimal (ex: 5% is 0.05)

0.05

Please give the Maximum Missing Data Level per marker (calculated at the Overall Population Level) in decimal (ex: 10% is 0.1)

0.1

Select designated Sample for Parent A

MB\_040

Select designated Sample for Parent B

MB\_040

Download JoinMap .Loc Input File (May take a min. Do not click more than once)

Download .Loc File

C

Select designated Sample for Parent A

MB\_040

MB\_040

MB\_048

Mac7 1238 Plt 199-2

Mac7 0238 Field 2012 Plot 0266

Mac7 1238 JS 1270-8 2015 0914 Plt1

MD26ne Plt 199-1

Mac7 0238 Plt 200

Mac7 1238 Plt 201

take a min. Do not click more than once)

Download Markers

Download Graph

Download Graph Data

# iCottonQTL

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Simple Steps Github Link

### Extended Steps Github Link

## Generate Input File for JoinMap

## CottonGen Upload Format

**Choose CSV File**

Browse...

No file selected

Optional: Choose TXT File Containing List of Sample Names

Browse...

No file selected

Please give the unique name for your dataset

TAMU SNP63K genotype

Download

Upload Final Report to the server and click download. This app will convert the genomic SNP data to IUPAC nomenclature and output a csv in the format required to submission to CottonGen.

User will need to open the downloaded file to input the species name for each sample under the 'species' column.

The screenshot displays the Microsoft Excel application window. The 'Home' tab is active, showing the ribbon with options for Font, Alignment, and Number. The spreadsheet contains a dataset with the following columns: A, B, C, D, E, F, G, and H. The data is organized into rows, with the first row (row 1) containing headers. The subsequent rows (rows 2-12) contain data entries. The data includes sample IDs, species names, and various identifiers. The interface shows the 'Home' tab with options for font, alignment, and number formatting.

	A	B	C	D	E	F	G	H
1	dataset_name	stock_name	genus	species	i00002Gh	i00003Gh	i00004Gh	i00005Gh
2	test_dataset	MB_040	Gossypium	T	C	T	T	G
3	test_dataset	MB_048	Gossypium	T	C	T	T	
4	test_dataset	Mac7 1238 Plt 199-2	Gossypium	T	C	T	T	
5	test_dataset	Mac7 0238 Field 2012 Plot 0266	Gossypium	T	C	T	T	
6	test_dataset	Mac7 1238 JS 1270-8 2015 0914 Plt1	Gossypium	T	C	T	T	
7	test_dataset	MD26ne Plt 199-1	Gossypium	T	C	T	T	G
8	test_dataset	Mac7 0238 Plt 200	Gossypium	T	C	T	T	G
9	test_dataset	Mac7 1238 Plt 201	Gossypium	T	C	T	T	
10	test_dataset	Mac7 0238 JS 1272-8, 2015 Plot 2221 Plt2	Gossypium	T	C	T	T	
11	test_dataset	TX 1145 Plt 204	Gossypium	T	C	T	T	
12	test_dataset	TX1214 Plt 202	Gossypium	T	C	T	T	

Please email the completed file to: [jing.yu@wsu.edu](mailto:jing.yu@wsu.edu)

 Click to Open Email